

10 30 50
 CATGGGTGGGGGTGGGGGCGCTGCTGGATTCTGCTCTGGTGGAGGGGAACTTGTGAGG
 70 90 110
 GGCTGGTAAGCGCCCCCTCCGAAGCCTGGTGTGTGCGCGGGGGAAGGAAGTTAGTTTCC
 130 150 170
 TCTCCACCCATGGGCACCCCTTCTGCCCGGGGCTGGGAAGTGGGCTGCTCTGTGGGCAA
 190 210 230
 ATGCTGGGGCCTCTGAAATGGAGGAGACGCAGCAGGGAGAGGCCCCACGTGGGCAGCTGC
 M E E T Q Q G E A P R G O L R
 250 270 290
 GCGGAGAGTCAGCAGCACCTGTCCCCCAGGCGCTCCTCCTGGTGTGCTGGGGGCGCGGG
 G E S A A P V P Q A L L L V L L G A R A
 310 330 350
 CCCAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGAAGTCCACAAGAAGATTG
 Q G G T R S P R C D C A G D F H K K I G
 370 390 410
 GTCTGTTTGTGTGCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCCCTTGCACGGAGC
 L F C C R G C P A G H Y L K A P C T E P
 430 450 470
 CCTGCGGCAACTCCACCTGCCTTGTGTGTCCCAAGACACCTTCTTGGCCTGGGAGAACC
 C G N S T C L V C P Q D T F L A W E N H
 490 510 530
 ACCATAATTCTGAATGTGCCCCGCTGCCAGGCCTGTGATGAGCAGGCCTCCCAGGTGGCGC
 H N S E C A R C Q A C D E Q A S Q V A L
 550 570 590
 TGGAGAAGTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAGCCAGGCTGGTTTGTGG
 E N C S A V A D T R C G C K P G W F V E
 610 630 650
 AGTGCCAGGTGAGCCAATGTGTGTCAGCAGTTACCCCTTCTACTGCCAACCATGCCTAGACT
 C Q V S Q C V S S S P F Y C Q P C L D C
 670 690 710
 GCGGGGCCCTGCACCGCCACACACGGCTACTCTGTTCCCGCAGAGATACTGACTGTGGGA
 G A L H R H T R L L C S R R D T D C G T
 730 750 770
 CCTGCCTGCCTGGCTTCTATGAACATGGCGATGGCTGCGTGTCTGCCCCACGAGCACCC
 C L P G F Y E H G D G C V S C P T S T L
 790 810 830
 TGGGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGGAGGCAGATGTTCTGGGTCC
 G S C P E R C A A V C G W R Q M F W V O
 850 870 890
 AGGTGCTCCTGGCTGGCCTTGTGGTCCCCCTCCTGCTTGGGGCCACCCTGACCTACACAT
 V L L A G L V V P L L L G A T L T Y T Y
 910 930 950
 ACCGCCACTGCTGGCCTCACAAGCCCCCTGGTTACTGCAGATGAAGCTGGGATGGAGGCTC
 R H C W P H K P L V T A D E A G M E A L

FIGURE 1A

970 990 1010
 TGACCCACACCGGCCACCCATCTGTACCCCTTGGACAGCGCCACACCCCTTCTAGCAC
 T P P P A T H L S P L D S A H T L L A P

1030 1050 1070
 CTCTGACAGCAGTGAGAAGATCTGCACCGTCCAGTTGGTGGGTAACAGCTGGACCCCTG
 P D S S E K I C T V Q L V G N S W T P G

1090 1110 1130
 GCTACCCCGAGACCCAGGAGGCGCTCTGCCCGCAGGTGACATGGTCCTGGGACCAGTTGC
 Y P E T Q E A L C P Q V T W S W D Q L P

1150 1170 1190
 CCAGCAGAGCTCTTGGCCCCGCTGTGCGCCCACTCTCGCCAGAGTCCCCAGCCGGCT
 S R A L G P A A A P T L S P E S P A G S

1210 1230 1250
 CGCCAGCATGATGCTGCAGCCGGGCGCGCAGCTCTACGACGTGATGGACGCGGTCCAG
 P A M M L Q P G P Q L Y D V M D A Y P A

1270 1290 1310
 CGCGGCGCTGGAAGGAGTTCTGTCGCAAGCTGGGGCTGCGCGAGGCAGATCGAAGCCG
R R W K E F V R T L G L R E A E I E A V

1330 1350 1370
 TGGAGGTGGAGATCGGCCGCTTCCGAGACCAGCAGTACGAGATGCTCAAGCGCTGGCGCC
E V E I G R F R D O O Y E M L K R W R O

1390 1410 1430
 AGCAGCAGCCCCGCGGGCCTCGGAGCCGTTTACGCGGCCCTGGAGCGCATGGGGCTGGACG
O O P A G L G A V Y A A L E R M G L D G

1450 1470 1490
 GCTGCGTGAAGACTTGCGCAGCCGCTGCGAGCGGGCCCGTGACACGGCGCCCACTTGC
C V E D L R S R L Q R G P *

1510 1530 1550
 CACCTAGGCGCTCTGGTGGCCCTTGCAAGAAGCCCTAAGTACGGTTACTTATGCGTGTAGA

1570 1590 1610
 CATTTTATGTCACTTTTAAAGCCGCTGGCACGGCCCTGCGTAGCAGCACCAGCCGGCCCC

1630 1650 1670
 ACCCCTGCTCGCCCCTATCGCTCCAGCCAAGGCGAAGAAGCACGAACGAATGTCGAGAGG

1690 1710 1730
 GGGTGAAGACATTTCTCAACTTCTCGGCCGGAGTTTGGCTGAGATCGCGGTATTAAATCT

1750 1770
 GTGAAAGAAAACAAAACAAAACAAAAAAAAAAAAAAAAAAAAA

FIGURE 1B

```

1  ATGGAGCAGC GGCCGCGGGG CTGCGCGGCG GTGGCGGCGG CGCTCCTCCT GGTGCTGCTG
   M E Q R P R G C A A V A A A L L L V L L
61  GGGGCCCCGG CCCAGGGCGG CACTCGTAGC CCCAGGTGTG ACTGTGCCGG TGACTTCCAC
   G A R A Q G G T R S P R C D C A G D F H
121 AAGAAGATTG GTCTGTTTGT TTGCAGAGGC TGCCCAGCGG GGCCTACCT GAAGGCCCTT
   K K I G L F C C R G C P A G H Y L K A P
181 TGCACGGAGC CCTGCGGCAA CTCCACCTGC CTTGTGTGTC CCCAAGACAC CTTCTTGGCC
   C T E P C G N S T C L V C P Q D T F L A
241 TGGGAGAACC ACCATAATTC TGAATGTGCC CGCTGCCAGG CCTGTGATGA GCAGGCCTCC
   W E N H H N S E C A R C Q A C D E Q A S
301 CAGGTGGCGC TGGAGAACTG TTCAGCAGTG GCCGACACCC GCTGTGGCTG TAAGCCAGGC
   Q V A L E N C S A V A D T R C G C K P G
361 TGGTTTGTGG AGTGCCAGGT CAGCCAATGT GTCAGCAGTT CACCCTTCTA CTGCCAACCA
   W F V E C Q V S Q C V S S S P F Y C Q P
421 TGCCTAGACT GCGGGGCCCT GCACCGCCAC ACACGGCTAC TCTGTTCCCG CAGAGATACT
   C L D C G A L H R H T R L L C S R R D T
481 GACTGTGGGA CCTGCCTGCC TGGCTTCTAT GAACATGGCG ATGGCTGCGT GTCCTGCCCC
   D C G T C L P G F Y E H G D G C V S C P
541 ACGAGCACCC TGGGGAGCTG TCCAGAGCGC TGTGCCGCTG TCTGTGGCTG GAGGCAGATG
   T S T L G S C P E R C A A V C G W R Q M
601 TTCTGGGTCC AGGTGCTCCT GGCTGGCCTT GTGGTCCCCC TCCTGCTTGG GGCCACCCTG
   F W V Q V L L A G L V V P L L L G A T L
661 ACCTACACAT ACCGCCACTG CTGGCCTCAC AAGCCCCCTG TTACTGCAGA TGAAGCTGGG
   T Y T Y R H C W P H K P L V T A D E A G
721 ATGGAGGCTC TGACCCCACC ACCGGCCACC CATCTGTCAC CCTTGGACAG CGCCACACC
   M E A L T P P P A T H L S P L D S A H T
781 CTTCTAGCAC CTCCTGACAG CAGTGAGAAG ATCTGCACCG TCCAGTTGGT GGGTAACAGC
   L L A P P D S S E K I C T V Q L V G N S
841 TGGACCCCTG GCTACCCCGA GACCCAGGAG GCGCTCTGCC CGCAGGTGAC ATGGTCCTGG
   W T P G Y P E T Q E A L C P Q V T W S W
901 GACCAGTTGC CCAGCAGAGC TCTTGGCCCC GCTGCTGCGC CCACACTCTC GCCAGAGTCC
   D Q L P S R A L G P A A A P T L S P E S
961 CCAGCCGGCT CGCCAGCCAT GATGCTGCAG CCGGGCCCGC AGCTCTACGA CGTGATGGAC
   P A G S P A M M L Q P G P Q L Y D V M D
1021 GCGGTCCCAG CGCGGCGCTG GAAGGAGTTC GTGCGCACGC TGGGGCTGCG CGAGGCAGAG
   A V P A R R W K E F V R T L G L R E A E
1081 ATCGAAGCCG TGGAGGTGGA GATCGGCCGC TTCCGAGACC AGCAGTACGA GATGCTCAAG
   I E A V E V E I G R F R D Q Q Y E M L K
1141 CGCTGGCGCC AGCAGCAGCC CGCGGGCCTC GGAGCCGTTT ACGCGGCCCT GGAGCGCATG
   R W R Q Q Q P A G L G A V Y A A L E R M
1201 GGGCTGGACG GCTGCGTGGA AGACTTGCGC AGCCGCTGC AGCGCGGCCC GTGA
   G L D G C V E D L R S R L Q R G P

```

FIGURE 2

Consensus #1	M	
DDCR	M E E T Q Q G E A P R G Q L R G E S A A P V P Q A L L L V L	30
TNFR1	M G L S T V P D L L L P L V L L E L L V G I Y P S G V I G L	30
FAS	M - L G I W T L L P L V L T S V A R L S S K S V N A Q V T D	29
Consensus #1 C	
DDCR	L G A R A Q G G T R S P R C D C A G D F H - - K K I G L F C	58
TNFR1	V P H L G D R E K R D S V C P Q G K Y I H - - P Q N N S I C	58
FAS	I N S K G L E L R K T V T T V E T Q N L E G L H H D G Q F C	59
Consensus #1	. . . C . . G C C . . C . . .	
DDCR	C R G C P A G H Y L K A P C T E P C G N S T C L V C P Q D T	88
TNFR1	C T K C H K G T Y L Y N D C P G P G Q D T D C R E C E S G S	88
FAS	H K P C P P G E R K A R D C T V N G D E P D C V P C Q E G K	89
Consensus #1 H . . . C . . C . . C C	
DDCR	F L A W E N H H N S E C A R C Q A C D E Q A S Q V A L E N C	118
TNFR1	F T A S E N H L R - H C L S C S K C R K E M G Q V E I S S C	117
FAS	E Y T D K A H F S S K C R R C R L C D E G H G L E V E I N C	119
Consensus #1 T . C . C	
DDCR	S A V A D T R C G C K P G W F V E C - - - Q V S Q C V S S S	145
TNFR1	T V D R D T V C G C R K N Q Y R H Y W S E N L F O C - - -	144
FAS	T R T Q N T K C R C K P N F F Q N - - - - - - - - -	137
Consensus #1 C	
DDCR	P F Y C Q P C L D C G A L H R H T R L L C S R R D T D C G T	175
TNFR1	- F N C S L C L N - G T V H - - - L S C Q E K Q N T V C T	167
FAS	- - - S T V C E H C D P - - - - - - - - - C T K	148
Consensus #1	C . . G C C . .	
DDCR	C L P G F Y E H G D G C V S C P T S T L G - S C P E R C - -	203
TNFR1	C H A G F F L R E N E C V S C S N C K K S L E C T K L C L P	197
FAS	C E H G I I - - - K E C - - - - - - - - - T L T S N T K C - -	166
Consensus #1	. L	
DDCR	- - - - - A A V C G W R Q M F W V Q V L L A G L V V P L	225
TNFR1	Q I E N V K G T E D S G T T V L L P L V I F F G L C L L S L	227
FAS	- - - - - K E E G S R S N L G W L C L L L - - L P I P L	186
Consensus #1	. .	
DDCR	L L G G T L D L H I P P L L A H K P L V T A D E A G M E A L	255
TNFR1	L F I G - L M Y R Y Q R W K S K L Y S I V C G K S T P E K E	256
FAS	I V - - - - - W V K R K E V - - - Q K T C R K H R	203
Consensus #1 G P	
DDCR	N P P P G T H L S P L D S A H T L L A P P D S S E K I C T V	285
TNFR1	G E L E G T T T K P L A P N P S F S P T P G F T P T L G F S	286
FAS	K E N Q G S H E S P - - - - - - - - - - -	214

FIGURE 3

Consensus #1

DDCR Q L V G N S W T P G Y P E T Q E A L C P Q V T W S W D Q L - 315
 TNFR1 P V P S S T F T S S S T Y T P G D - C P N F A A P R R E V A 315
 FAS - - - - - 214

Consensus #1 L

DDCR - P S R A L G P A A A P T L S P E S P A G S - - - - - 336
 TNFR1 P P Y Q G A D P I L A T A L A S D P I P N P L Q K W E D S A 345
 FAS - - - - - T L N P E T V A I N L S - - - - - 226

Consensus #1 K . F V

DDCR - - - P A M M L O P G P Q L Y D V M D A V P A R R W K E F V 362
 TNFR1 H K P Q S L D T D D P A T L Y A V V E N V P P L R W K E F V 375
 FAS - - - - - D V D L S K Y I T T I A G V M T L S Q V K G E F V 249

Consensus #1 R I L .

DDCR R T L G L R E A E I E A V E V E I C R - F R D Q Q Y E M L K 391
 TNFR1 R R L G L S D H E I D R L E L Q N C R C L R E A Q Y S M L A 405
 FAS R K N G V N E A K I D E I K N D N V Q D T A E Q K V Q L L R 279

Consensus #1 . W A L E

DDCR R W R Q Q Q P - - - A G L G A V Y A A L E R M G L D C C V E 418
 TNFR1 T W R R R T P R R E A T L E L L G R V L R D M D L L C C L E 435
 FAS N W H Q L H G K K E A - Y D T L I K D L K K A N L C T L A E 308

Consensus #1

DDCR D L - - - - - R S R L Q R G P 428
 TNFR1 D T E E A L - - - - - C G P A A L P P A P S L L R 455
 FAS K T Q T I I L K D I T S D S E N S N F R N E I Q S L V 335

Consensus 'Consensus #1': When all match the residue of the Consensus show the residue of the Consensus, otherwise show '.'.

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

FIGURE 3 (CONT'D)

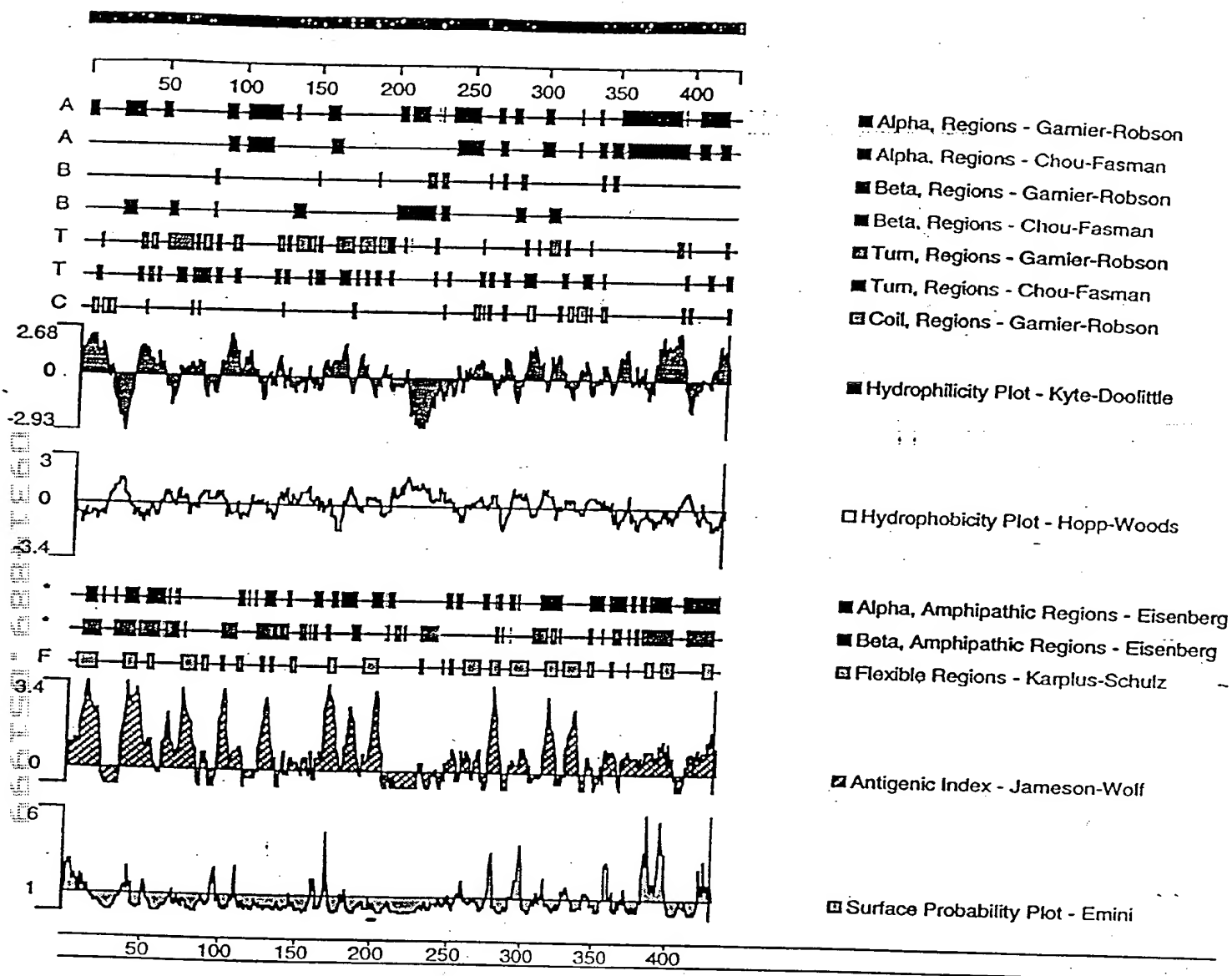


FIGURE 4